



IFWO

RAW SEQUENCE LISTING
 PATENT APPLICATION: US/10/724,301

DATE: 08/02/2004
 TIME: 15:07:13

Input Set : A:\1-1411 SEQUENCE LISTING.txt
 Output Set: N:\CRF4\08022004\J724301.raw

3 <110> APPLICANT: Enenkel, Barbara
 4 Fieder, Juergen
 5 Otto, Ralf
 6 Sautter, Kerstin
 7 Bergemann, Klaus
 9 <120> TITLE OF INVENTION: Neomycin-Phosphotransferase Genes and Methods
 10 for the Selection of Recombinant Cells Producing
 11 High Levels of a Desired Gene Product
 13 <130> FILE REFERENCE: 1/1411
 C--> 15 <140> CURRENT APPLICATION NUMBER: US/10/724,301
 16 <141> CURRENT FILING DATE: 2003-11-26
 18 <150> PRIOR APPLICATION NUMBER: US 60/431,535
 19 <151> PRIOR FILING DATE: 2002-12-06
 21 <150> PRIOR APPLICATION NUMBER: US 60/487,902
 22 <151> PRIOR FILING DATE: 2003-07-17
 24 <150> PRIOR APPLICATION NUMBER: DE 102 56 081
 25 <151> PRIOR FILING DATE: 2002-11-29
 27 <150> PRIOR APPLICATION NUMBER: DE 103 30 686
 28 <151> PRIOR FILING DATE: 2003-07-08
 30 <160> NUMBER OF SEQ ID NOS: 55
 32 <170> SOFTWARE: PatentIn Ver. 3.1
 34 <210> SEQ ID NO: 1
 35 <211> LENGTH: 795
 36 <212> TYPE: DNA
 37 <213> ORGANISM: Escherichia coli
 39 <400> SEQUENCE: 1
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 41 ggctatgact gggcacaca gacaatcgcc tgctctgatg ccggcgtgtt ccggctgtca 120
 42 ggcgcaggggc gcccgggtct ttttgcggat accgacgtt ccggctgtcc 180
 43 caagacgagg cagcgcgcgt atcgtggctg gccacgcgg gcgttccctg cgcagctgtg 240
 44 ctcgacgttg tcactgaagc gggaaaggac tggctgtat tggcgaagt gcccggcag 300
 45 gatctcctgt catctcacct tgctcctgcc gagaaagat ccatcatggc tgatgcaatg 360
 46 cggcggctgc atacgcttgc tccggctacc tgcccatcg accaccaagc gaaacatcg 420
 47 atcgagcgag cacgtactcg gatggaaagcc ggtcttgctcg atcaggatga tctggacgaa 480
 48 gagcatcagg ggctcgcc agccgaactg ttgcggcaggc tcaaggcggag catgcccac 540
 49 ggcgaggatc tgcgtgtac ccatggcgat gcctgctgc cgaatatcat ggtggaaaat 600
 50 ggccgcgttt ctggattcat cgactgtggc cggctgggtg tggcggaccg ctatcaggac 660
 51 atagcggtgg ctacccgtga tattgctgaa gagcttggcg gcaatgggc tgaccgttc 720
 52 ctcgtgttt acggtatcgcc cgctcccgat tcgcagcgc tgccttcta tcgccttctt 780
 53 gacgagttct tctga 795
 56 <210> SEQ ID NO: 2
 57 <211> LENGTH: 264
 58 <212> TYPE: PRT



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59 <213> ORGANISM: Escherichia coli
 61 <400> SEQUENCE: 2
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 63 1 5 10 15
 65 Glu Arg Leu Phe Gly Tyr Asp Trp Ala Gln Gln Thr Ile Gly Cys Ser
 66 20 25 30
 68 Asp Ala Ala Val Phe Arg Leu Ser Ala Gln Gly Arg Pro Val Leu Phe
 69 35 40 45
 71 Val Lys Thr Asp Leu Ser Gly Ala Leu Asn Glu Leu Gln Asp Glu Ala
 72 50 55 60
 74 Ala Arg Leu Ser Trp Leu Ala Thr Thr Gly Val Pro Cys Ala Ala Val
 75 65 70 75 80
 77 Leu Asp Val Val Thr Glu Ala Gly Arg Asp Trp Leu Leu Gly Glu
 78 85 90 95
 80 Val Pro Gly Gln Asp Leu Leu Ser Ser His Leu Ala Pro Ala Glu Lys
 81 100 105 110
 83 Val Ser Ile Met Ala Asp Ala Met Arg Arg Leu His Thr Leu Asp Pro
 84 115 120 125
 86 Ala Thr Cys Pro Phe Asp His Gln Ala Lys His Arg Ile Glu Arg Ala
 87 130 135 140
 89 Arg Thr Arg Met Glu Ala Gly Leu Val Asp Gln Asp Asp Leu Asp Glu
 90 145 150 155 160
 92 Glu His Gln Gly Leu Ala Pro Ala Glu Leu Phe Ala Arg Leu Lys Ala
 93 165 170 175
 95 Ser Met Pro Asp Gly Glu Asp Leu Val Val Thr His Gly Asp Ala Cys
 96 180 185 190
 98 Leu Pro Asn Ile Met Val Glu Asn Gly Arg Phe Ser Gly Phe Ile Asp
 99 195 200 205
 101 Cys Gly Arg Leu Gly Val Ala Asp Arg Tyr Gln Asp Ile Ala Leu Ala
 102 210 215 220
 104 Thr Arg Asp Ile Ala Glu Glu Leu Gly Gly Glu Trp Ala Asp Arg Phe
 105 225 230 235 240
 107 Leu Val Leu Tyr Gly Ile Ala Ala Pro Asp Ser Gln Arg Ile Ala Phe
 108 245 250 255
 110 Tyr Arg Leu Leu Asp Glu Phe Phe
 111 260
 114 <210> SEQ ID NO: 3
 115 <211> LENGTH: 795
 116 <212> TYPE: DNA
 117 <213> ORGANISM: Artificial sequence
 119 <220> FEATURE:
 120 <223> OTHER INFORMATION: Neomycin mutant E182G
 122 <400> SEQUENCE: 3
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 124 ggctatgact gggcacaaca gacaatggc tgctctgatg cgcgcgtgtt ccggctgtca 120
 125 ggcgcaggggc gccegggtct ttttgtcaag accgacactgt ccgggtccctt gaatgaactg 180
 126 caagacgagg cagcgcggct atcgtggctg gccacgacgg gcgttccctg cgcagctgtg 240
 127 ctcgacgttg tcaactgaagc gggaaaggac tggctgtat tgggcgaagt gcccggcag 300
 128 gatctcctgt catctcacct tgctcctgcc gagaaagtat ccatcatggc tcatgcattg 360

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129 cgccggctgc atacgcttga tccggctacc tgcccattcg accaccaagc gaaacatcgc 420
 130 atcgagcgag cacgtactcg gatggaaagcc ggtcttgcg atcaggatga tctggacgaa 480
 131 gacgatcagg ggctcgccgc agccgaactg ttcgcccaggc tcaaggcggag catgcccac 540
 132 ggcggggatc tcgtcggtac ccattggcgat gcctgcttgc cgaatatcat ggtggaaaat 600
 133 ggccgcgttt ctggattcat cgactgtggc cggctgggtg tggcggaccc ctatcaggac 660
 134 atagcggtgg ctaccgtga tattgtgaa gagctggcg gcaatgggc tgaccgcttc 720
 135 ctcgtgtttt acggatcgcc cgctcccgat tcgcagcgc tcgccttcta tcgccttctt 780
 136 gacgagttct tctga 795
 139 <210> SEQ ID NO: 4
 140 <211> LENGTH: 264
 141 <212> TYPE: PRT
 142 <213> ORGANISM: Artificial sequence
 144 <220> FEATURE:
 145 <223> OTHER INFORMATION: Neomycin mutant E182G
 147 <400> SEQUENCE: 4
 148 Met Ile Glu Gln Asp Gly Leu His Ala Gly Ser Pro Ala Ala Trp Val
 149 1 5 10 15
 151 Glu Arg Leu Phe Gly Tyr Asp Trp Ala Gln Gln Thr Ile Gly Cys Ser
 152 20 25 30
 154 Asp Ala Ala Val Phe Arg Leu Ser Ala Gln Gly Arg Pro Val Leu Phe
 155 35 40 45
 157 Val Lys Thr Asp Leu Ser Gly Ala Leu Asn Glu Leu Gln Asp Glu Ala
 158 50 55 60
 160 Ala Arg Leu Ser Trp Leu Ala Thr Thr Gly Val Pro Cys Ala Ala Val
 161 65 70 75 80
 163 Leu Asp Val Val Thr Glu Ala Gly Arg Asp Trp Leu Leu Leu Gly Glu
 164 85 90 95
 166 Val Pro Gly Gln Asp Leu Leu Ser Ser His Leu Ala Pro Ala Glu Lys
 167 100 105 110
 169 Val Ser Ile Met Ala Asp Ala Met Arg Arg Leu His Thr Leu Asp Pro
 170 115 120 125
 172 Ala Thr Cys Pro Phe Asp His Gln Ala Lys His Arg Ile Glu Arg Ala
 173 130 135 140
 175 Arg Thr Arg Met Glu Ala Gly Leu Val Asp Gln Asp Asp Leu Asp Glu
 176 145 150 155 160
 178 Glu His Gln Gly Leu Ala Pro Ala Glu Leu Phe Ala Arg Leu Lys Ala
 179 165 170 175
 181 Ser Met Pro Asp Gly Gly Asp Leu Val Val Thr His Gly Asp Ala Cys
 182 180 185 190
 184 Leu Pro Asn Ile Met Val Glu Asn Gly Arg Phe Ser Gly Phe Ile Asp
 185 195 200 205
 187 Cys Gly Arg Leu Gly Val Ala Asp Arg Tyr Gln Asp Ile Ala Leu Ala
 188 210 215 220
 190 Thr Arg Asp Ile Ala Glu Leu Gly Glu Trp Ala Asp Arg Phe
 191 225 230 235 240
 193 Leu Val Leu Tyr Gly Ile Ala Ala Pro Asp Ser Gln Arg Ile Ala Phe
 194 245 250 255
 196 Tyr Arg Leu Leu Asp Glu Phe Phe
 197 260

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200 <210> SEQ ID NO: 5
 201 <211> LENGTH: 795
 202 <212> TYPE: DNA
 203 <213> ORGANISM: Artificial sequence
 205 <220> FEATURE:
 206 <223> OTHER INFORMATION: Neomycin mutant W91A
 208 <400> SEQUENCE: 5
 209 atgattgaac aagatggatt gcacgcagg tctccggccg cttgggtgga gaggctattc 60
 210 ggctatgact gggcacaaca gacaatcgcc tgctctgatg ccggcgtgtt ccggctgtca 120
 211 gcgcaggggc gccccgttct ttttgtcaag accgacctgt ccgggtccct gaatgaactg 180
 212 caagacgagg cagcgggct atcgtggctg gccacgacgg gcgttccctt cgcagctgtg 240
 213 ctcgacgttg tcactgaagc gggaaaggac gcgctgtat tggcgaagt gccggggcag 300
 214 gatctcctgt catctcacct tgctcctgcc gagaaagtat ccatcatggc tcatgcaatg 360
 215 cggcggctgc atacgcttga tccggctacc tgcccatcgc accaccaagg gaaacatcgc 420
 216 atcgagcggag cacgtactcg gatggaaagcc ggtcttgctg atcaggatga tctggacgaa 480
 217 gagcatcagg ggctcgcgc agccgaactg ttgcgcaggc tcaaggcggag catgcccgc 540
 218 ggcgaggatc tcgtcgtgac ccatggcgat gcctgcttgc cgaatatcat ggtggaaaat 600
 219 ggcgcgtttt ctggattcat cgactgtggc cggctgggtg tggcggaccc ctatcaggac 660
 220 atagcggttgg ctacccgtga tattgctgaa gagcttggcg gcaatgggc tgaccgcttc 720
 221 ctcgtgtttt acggtatcgc cgctcccgat tcgcagcgc tcgccttcta tcgccttctt 780
 222 gacgagttct tctga 795
 225 <210> SEQ ID NO: 6
 226 <211> LENGTH: 264
 227 <212> TYPE: PRT
 228 <213> ORGANISM: Artificial sequence
 230 <220> FEATURE:
 231 <223> OTHER INFORMATION: Neomycin mutant W91A
 233 <400> SEQUENCE: 6
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 237 Glu Arg Leu Phe Gly Tyr Asp Trp Ala Gln Gln Thr Ile Gly Cys Ser
 238 20 25 30
 240 Asp Ala Ala Val Phe Arg Leu Ser Ala Gln Gly Arg Pro Val Leu Phe
 241 35 40 45
 243 Val Lys Thr Asp Leu Ser Gly Ala Leu Asn Glu Leu Gln Asp Glu Ala
 244 50 55 60
 246 Ala Arg Leu Ser Trp Leu Ala Thr Thr Gly Val Pro Cys Ala Ala Val
 247 65 70 75 80
 249 Leu Asp Val Val Thr Glu Ala Gly Arg Asp Ala Leu Leu Leu Gly Glu
 250 85 90 95
 252 Val Pro Gly Gln Asp Leu Leu Ser Ser His Leu Ala Pro Ala Glu Lys
 253 100 105 110
 255 Val Ser Ile Met Ala Asp Ala Met Arg Arg Leu His Thr Leu Asp Pro
 256 115 120 125
 258 Ala Thr Cys Pro Phe Asp His Gln Ala Lys His Arg Ile Glu Arg Ala
 259 130 135 140
 261 Arg Thr Arg Met Glu Ala Gly Leu Val Asp Gln Asp Asp Leu Asp Glu
 262 145 150 155 160
 264 Glu His Gln Gly Leu Ala Pro Ala Glu Leu Phe Ala Arg Leu Lys Ala

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265	165	170	175	
267	Ser Met Pro Asp Gly Glu Asp Leu Val Val Thr His Gly Asp Ala Cys			
268	180	185	190	
270	Leu Pro Asn Ile Met Val Glu Asn Gly Arg Phe Ser Gly Phe Ile Asp			
271	195	200	205	
273	Cys Gly Arg Leu Gly Val Ala Asp Arg Tyr Gln Asp Ile Ala Leu Ala			
274	210	215	220	
276	Thr Arg Asp Ile Ala Glu Glu Leu Gly Gly Glu Trp Ala Asp Arg Phe			
277	225	230	235	240
279	Leu Val Leu Tyr Gly Ile Ala Ala Pro Asp Ser Gln Arg Ile Ala Phe			
280	245	250	255	
282	Tyr Arg Leu Leu Asp Glu Phe Phe			
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287	<211> LENGTH: 795			
288	<212> TYPE: DNA			
289	<213> ORGANISM: Artificial sequence			
291	<220> FEATURE:			
292	<223> OTHER INFORMATION: Neomycin mutant V198G			
294	<400> SEQUENCE: 7			
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297	gcgcaggggc gcccgggtct ttttgtcaag accgacctgt ccgggtgcctt gaatgaactg 180			
298	caagacgagg cagcgcggct atcgtggctg gccacgacgg gcgttccttg cgcagctgtg 240			
299	ctcgacgttg tcaactgaagc gggaaaggac tggctgctat tggcgaagt gccggggcag 300			
300	gatctctgt catctcacct tgctcctgcc gagaaaggat ccatcatggc tgatgcaatg 360			
301	cggcggctgc atacgcttga tccggctacc tgcccatcg accaccaagc gaaacatcgc 420			
302	atcgagcggag cacgtactcg gatggaaagcc ggtcttgcg atcaggatga tctggacgaa 480			
303	gagcatcagg ggctcgcggc agccgaactg ttcggcaggc tcaaggcgg catgcccac 540			
304	ggcgaggatc tgcgtcgac ccatggcgat gcctgttgc cgaatatcat gggggaaaat 600			
305	ggccgctttt ctggattcat cgactgtggc cggctgggtg tggcggaccc ctatcaggac 660			
306	atagcgttgg ctacccgtga tattgctgaa gagcttggcg gcaatgggc tgaccgccttc 720			
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312	<211> LENGTH: 264			
313	<212> TYPE: PRT			
314	<213> ORGANISM: Artificial sequence			
316	<220> FEATURE:			
317	<223> OTHER INFORMATION: Neomycin mutant V198G			
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323	Glu Arg Leu Phe Gly Tyr Asp Trp Ala Gln Gln Thr Ile Gly Cys Ser			
324	20 25 30			
326	Asp Ala Ala Val Phe Arg Leu Ser Ala Gln Gly Arg Pro Val Leu Phe			
327	35 40 45			
329	Val Lys Thr Asp Leu Ser Gly Ala Leu Asn Glu Leu Gln Asp Glu Ala			
330	50 55 60			

VERIFICATION SUMMARY

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L:15 M:270 C: Current Application Number differs, Replaced Current Application Number